ALSTON & BIRD

TEL:9198622260

P. 023

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InterPro: DNA mismatch repair protein



InterPro: DNA mismatch repair protein

Pags 2 of 2

P54279	PMS2_MOUSE	Mouse proetin PSM2	
P14161	MUTL_SALTY	mutL bacterial proteil	n
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		Tillunian III.	
P14160	HEXB STRPN	Streptococcus pneun	noniae hexB protein
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Property Mariles (4) (4) (4)			
P40692	MLH1_HUMAN	Human protein MLH1	
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- In- I strat bishe at a strain of the			

More proteins...

IPR002099 DNA mismatch repair protein
IPR003594 ATP-binding region, ATPase-like
SuperFamily

Publications

1. Modrich P.

DNA mismatch correction.

Annu. Rev. Biochem. 56: 435- 466 (1987) [PubMed: 3304141]

2. McIntyre C.A., Mankovich J.A., Walker G.C.

Nucleotide sequence of the Salmonella typhimurlum mutL gene required for mismatch repair: homology of MutL to HexB of Streptococcus pneumoniae and to PMS1 of the yeast Saccharomyces cerevisiae.

- J. Bacteriol. 171: 5325- 5331 (1989) [PubMed: 2676972]
- 3. Prudhomme M., Claverys J.-P., Mejean V., Martin B.

Nucleotide sequence of the Streptococcus pneumoniae hexB mismatch repair gene: homology of HexB to MutL of Salmonella typhimurium and to PMS1 of Saccharomyces cerevisiae.

- J. Bacteriol. 171: 5332- 6338 (1989) [PubMed: 2676973]
- Bronner C.E., Godwin A.R., Tannergard P., Linblom A., Bollag R.J., Lipford J., Warren G., Earibino C., Karle M., 4. Lescoe M.K., Kolodner R.D., Smith L.G., Fishel R., Morrison P.T., Baker S.M., Nordenskjold M., Liskay R.M., Ward D.C.

Mutation in the DNA mismatch repair gene homologue hMLH1 is associated with hereditary non-polyposis colorcancer.

Nature 368: 258- 261 (1994) [PubMed: 8145827]

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InterProScan



Get Nucleotide sequences 🖫 (or

SHS SHE 7 Sile search

> REPLACE

INTERPRO DATABASE

InterProScan Results

'n.,..

Pieme Vew	

DNA mismatch repair protein, C-termina SEQUENCE: Sequence 1 CRC64: 245289C333C7D8AA LENGTH: 724 aa DNA mismatch repair protein TIGR00585 FF01119

muti: DNA mismatch repair protein MufiL DNA MISMATCH REPAIR PS00058

TIGREAMS

PFAM

²R002099

Pall Pall

InterPro

PROSITE no parent

E E

InterProScan Help

References

no children

Children

Parent

no entries IPR003594

Found in Contains

2.1e-39 [231-348]T 1e-118 [16-328]T NA (108-114)?

PACE 25/30 * RCVD AT 3/22/2004 6:14:00 PM [Eastern Standard Time] * SVR:USPTO-EFXRF-1/2 * DNIS:8729306 * CSID:9198622260 * DURATION (mm-5-5):14-36

0.00018 F33-167TT D.0052 [33-153]T

> Histidine kinase-, DNA gyrase B-, and Histidine kinase-like ATPases

PR001241 | PR001404 | PR002099 | PR005467 | PR005734 | PR006290 | PR008358 | PR010193

no entries

Found in Contains

PR004358 IPR010194

Children

no parent

Parent

unintegrated unintegrated

Molecular Function: ATP binding (GO:0005524)

GO terms

nolPR

LANCITHE

e-104 [27-208]

444. Hasta shi sa ukkati hirfimersanfimersan Phalzimersan Biakidzimersan 10041217.20469660 Sumdzahank Britaka

LET: 6168655560

• Help

General Help

Formats ₹ Gaps • Matrix

P' 052

ALSTON & BIRD

Biological Process: mismatch repair (GO:0006298)

GO terms

ATP-binding region, ATPase-like

SM00387

SMART

-

PFAM

PR003594

Jamain

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Productional Chargodoms

PAGE 26/30 * RCVD AT 3/22/2004 6:14:00 PM [Eastern Standard Time] * SVR:USPTO-EFXRF-1/2 * DNIS:8729306 * CSID:91986222560 * DURATION (mm-ss):14-56